

☆ Testosterone level (Ruth, 2020)

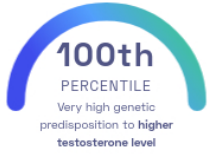
Katherine Ruth, et al.
Nature Medicine

Hormones Sex

STUDY SUMMARY

Identification of over 200 genetic variants associated with testosterone level.

YOUR RESULT



STUDY DESCRIPTION

Testosterone is the main male sex hormone. However, it regulates bodily functions, like muscle development and fertility, in both sexes. This study examined over 425,000 individuals of European ancestry from the UK Biobank database to identify genetic factors associated with testosterone level. The researchers linked over 200 genetic variants to testosterone level in both sexes. These variants explained 17% of the heritability of testosterone level in men and 13% of the heritability in women. The study also found differences between sexes with some variants showing opposite effect directions. Furthermore, the results of this study indicate that genetic predisposition to higher testosterone is beneficial to men but harmful to women. For example, genetically determined higher testosterone level in men decreased the risk of type 2 diabetes but increased that risk in women.

DID YOU KNOW?

For men, getting enough sleep and exercising regularly are two ways to naturally increase testosterone level without supplements.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher testosterone level we summed up the effects of genetic variants that were linked to higher testosterone level in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to higher testosterone level. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to higher testosterone level. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher testosterone level. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for higher testosterone level to be 4.08. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for higher testosterone level is in the 100th percentile. This means that it is higher than the polygenic scores 100% of people. We consider this to be a very high genetic predisposition to higher testosterone level. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

VARIANT [Ⓞ]	YOUR GENOTYPE [Ⓞ]	EFFECT SIZE [Ⓞ]	VARIANT FREQUENCY [Ⓞ]	SIGNIFICANCE [Ⓞ]
rs1799941_A	G / A	0.06 (↑)	26%	1.70 x 10 ⁻⁴²⁴
rs45446698_T	T / T	0.12 (↑)	96%	1.70 x 10 ⁻³¹⁶
rs10740131_T	T / T	0.04 (↑)	47%	2.50 x 10 ⁻¹⁹⁶
rs112265145_C	A / A	0.04 (-)	27%	3.00 x 10 ⁻¹⁸⁶
rs6258_C	C / C	0.22 (↑)	99%	4.60 x 10 ⁻¹⁷⁰
rs1673036_T	T / T	0.03 (↑)	39%	3.00 x 10 ⁻¹³⁶
rs1260326_C	C / C	0.03 (↑)	61%	3.50 x 10 ⁻¹⁰³
rs56196860_A	NA	0.06 (-)	3%	7.20 x 10 ⁻⁷¹
rs6684361_C	T / T	0.03 (-)	31%	2.50 x 10 ⁻⁷⁰
rs7183977_C	T / T	0.02 (-)	35%	3.10 x 10 ⁻⁵⁷
rs36032941_C	C / C	0.02 (↑)	70%	5.00 x 10 ⁻⁶⁶
rs9509847_C	C / A	0.02 (↑)	63%	1.60 x 10 ⁻⁵²
rs590097_G	T / G	0.02 (↑)	65%	3.80 x 10 ⁻⁴⁸
rs113017476_A	NA	0.05 (-)	4%	4.00 x 10 ⁻⁴⁷
rs79384925_C	C / C	0.03 (↑)	86%	2.00 x 10 ⁻⁴¹
rs17089026_G	NA	0.05 (-)	2%	7.10 x 10 ⁻³⁷
rs2061679_T	C / C	0.03 (-)	7%	1.50 x 10 ⁻³⁶
rs761180516_A	NA	0.21 (-)	< 1%	2.10 x 10 ⁻³⁶
rs56332871_A	C / C	0.02 (-)	27%	3.50 x 10 ⁻³⁴
rs1317701_C	C / C	0.02 (↑)	31%	3.70 x 10 ⁻³⁴
rs17853284_C	C / C	0.12 (↑)	> 99%	3.80 x 10 ⁻³⁴
rs2306847_T	T / T	0.02 (↑)	79%	5.20 x 10 ⁻³⁴
rs36182456_A	G / G	0.02 (-)	78%	2.10 x 10 ⁻³³
rs1171617_T	T / T	0.02 (↑)	77%	8.50 x 10 ⁻³¹
rs4632729_A	A / A	0.01 (↑)	55%	2.10 x 10 ⁻³⁰
rs146497684_T	NA	0.04 (-)	3%	1.20 x 10 ⁻²⁹
rs1977658_T	T / G	0.01 (↑)	34%	1.60 x 10 ⁻²⁷
rs2011425_T	T / T	0.03 (↑)	92%	3.10 x 10 ⁻²⁶
rs34060476_G	A / G	0.02 (↑)	13%	5.30 x 10 ⁻²⁶
rs12658172_G	G / G	0.02 (↑)	84%	2.70 x 10 ⁻²³
rs6458331_T	T / T	0.01 (↑)	73%	1.20 x 10 ⁻²²
rs171021_C	C / C	0.01 (↑)	70%	2.70 x 10 ⁻²¹

rs784420_G	G / G	0.01 (↑)	29%	3.20 × 10 ⁻²¹
rs738409_G	C / C	0.01 (-)	22%	7.40 × 10 ⁻²¹
rs74662944_C	NA	0.07 (-)	1%	2.50 × 10 ⁻²⁰
rs35783704_A	G / A	0.02 (↑)	10%	2.60 × 10 ⁻²⁰
rs9272309_A	G / G	0.01 (-)	62%	1.10 × 10 ⁻¹⁹
rs6471683_G	G / A	0.01 (↑)	44%	1.10 × 10 ⁻¹⁹
rs8111359_C	C / T	0.02 (↑)	91%	1.90 × 10 ⁻¹⁹
rs58839393_A	A / A	0.02 (↑)	84%	3.90 × 10 ⁻¹⁹
rs1408_G	A / A	0.01 (-)	42%	6.80 × 10 ⁻¹⁹
rs1204083_C	G / G	0.01 (-)	35%	2.80 × 10 ⁻¹⁸
rs2517582_T	T / T	0.01 (↑)	38%	4.90 × 10 ⁻¹⁸
rs7686914_C	C / C	0.01 (↑)	48%	9.20 × 10 ⁻¹⁸
rs28929474_T	NA	0.04 (-)	2%	1.10 × 10 ⁻¹⁷
rs4804669_A	G / G	0.01 (-)	22%	2.40 × 10 ⁻¹⁷
rs10892924_T	A / T	0.01 (↑)	57%	2.70 × 10 ⁻¹⁷
rs11673591_A	T / T	0.01 (-)	25%	4.80 × 10 ⁻¹⁷
rs10817260_C	C / C	0.01 (↑)	81%	6.90 × 10 ⁻¹⁷
rs35816571_C	C / C	0.01 (↑)	83%	1.40 × 10 ⁻¹⁶
rs78248023_A	C / C	0.02 (-)	8%	1.60 × 10 ⁻¹⁶
rs520829_G	G / G	0.01 (↑)	48%	2.20 × 10 ⁻¹⁶
rs11102518_T	T / T	0.01 (↑)	68%	2.70 × 10 ⁻¹⁶
rs4464040_C	C / C	0.01 (↑)	85%	2.80 × 10 ⁻¹⁶
rs61823391_T	T / C	0.01 (↑)	68%	4.20 × 10 ⁻¹⁶
rs782207398_T	TA / TA	0.01 (-)	67%	4.40 × 10 ⁻¹⁶
rs759068_A	G / G	0.01 (-)	29%	5.20 × 10 ⁻¹⁶
rs12436785_C	T / C	0.01 (↑)	42%	7.00 × 10 ⁻¹⁶
rs67967246_C	A / A	0.01 (-)	13%	9.20 × 10 ⁻¹⁶
rs73075656_G	G / G	0.01 (↑)	87%	2.10 × 10 ⁻¹⁵
rs61755050_T	T / T	0.06 (↑)	99%	2.80 × 10 ⁻¹⁵
rs6130613_T	C / C	0.01 (-)	47%	2.90 × 10 ⁻¹⁵
rs9913470_A	A / G	0.01 (↑)	80%	5.30 × 10 ⁻¹⁵
rs4453027_G	G / T	0.01 (↑)	57%	5.50 × 10 ⁻¹⁵
rs1547308_C	C / C	0.01 (↑)	80%	6.80 × 10 ⁻¹⁵
rs4431325_T	C / C	0.02 (-)	6%	9.90 × 10 ⁻¹⁵
rs2723065_G	A / G	0.01 (↑)	38%	1.30 × 10 ⁻¹⁴
rs9686661_C	C / C	0.01 (↑)	80%	1.30 × 10 ⁻¹⁴
rs10278686_T	T / T	0.01 (↑)	49%	1.30 × 10 ⁻¹⁴
rs56117787_G	A / A	0.01 (-)	20%	1.90 × 10 ⁻¹⁴
rs2903385_A	G / A	0.01 (↑)	49%	2.10 × 10 ⁻¹⁴
rs5752773_G	G / G	0.01 (↑)	33%	2.20 × 10 ⁻¹⁴
rs8126001_T	C / T	0.01 (↑)	49%	2.30 × 10 ⁻¹⁴
rs79391862_A	A / A	0.04 (↑)	99%	2.40 × 10 ⁻¹⁴
rs768863_T	G / G	0.01 (-)	50%	2.70 × 10 ⁻¹⁴
rs28421540_A	A / A	0.01 (↑)	72%	3.00 × 10 ⁻¹⁴
rs2241388_T	T / C	0.01 (↑)	28%	3.20 × 10 ⁻¹⁴
rs41378347_G	G / G	0.01 (↑)	89%	5.20 × 10 ⁻¹⁴
rs62115715_C	NA	0.03 (-)	3%	8.30 × 10 ⁻¹⁴
rs20111036_C	AGCCCTCAG / AGCCCTCAG	0.02 (-)	91%	1.10 × 10 ⁻¹³
rs36205397_G	A / G	0.01 (↑)	42%	1.30 × 10 ⁻¹³
rs7759938_T	T / T	0.01 (↑)	68%	1.70 × 10 ⁻¹³
rs12683780_A	A / A	0.01 (↑)	67%	2.80 × 10 ⁻¹³
rs111861797_T	T / C	0.01 (↑)	81%	3.30 × 10 ⁻¹³
rs112694713_A	A / A	0.04 (↑)	99%	3.50 × 10 ⁻¹³
rs1128249_T	G / T	0.01 (↑)	39%	4.10 × 10 ⁻¹³

rs7342537_G	NA	0.04 (-)	2%	5.60 x 10 ⁻¹⁰
rs138983180_A	NA	0.06 (-)	1%	6.60 x 10 ⁻¹³
rs10971921_A	G / G	0.01 (-)	13%	7.40 x 10 ⁻¹³
rs182050989_C	C / T	0.03 (↑)	97%	1.20 x 10 ⁻¹²
rs267733_A	A / A	0.01 (↑)	84%	1.20 x 10 ⁻¹²
rs28495625_A	C / C	0.01 (-)	15%	1.20 x 10 ⁻¹²
rs528845403_A	ATGTGT / ATGTGT	0.05 (-)	99%	1.40 x 10 ⁻¹²
rs5751229_A	G / G	0.01 (-)	23%	1.50 x 10 ⁻¹²
rs3771243_A	G / A	0.01 (↑)	39%	2.50 x 10 ⁻¹²
rs1870940_G	G / A	0.01 (↑)	73%	2.90 x 10 ⁻¹²
rs370222_G	G / A	0.01 (↑)	70%	3.10 x 10 ⁻¹²
rs4782568_G	C / G	0.01 (↑)	45%	3.90 x 10 ⁻¹²
rs73365510_A	G / G	0.02 (-)	7%	4.00 x 10 ⁻¹²
rs77017252_T	T / A	0.01 (↑)	76%	4.80 x 10 ⁻¹²
rs4678408_G	G / G	0.01 (↑)	63%	5.90 x 10 ⁻¹²
rs11191801_A	A / C	0.01 (↑)	71%	6.00 x 10 ⁻¹²
rs6020423_C	C / C	0.01 (↑)	76%	6.40 x 10 ⁻¹²
rs34955534_G	G / G	0.01 (↑)	90%	6.50 x 10 ⁻¹²
rs55707100_C	C / C	0.03 (↑)	98%	7.70 x 10 ⁻¹²
rs72681869_C	NA	0.04 (-)	1%	8.80 x 10 ⁻¹²
rs28576256_G	G / G	0.01 (↑)	87%	9.10 x 10 ⁻¹²
rs11023881_T	A / A	0.01 (-)	61%	1.70 x 10 ⁻¹¹
rs61320678_G	T / T	0.01 (-)	24%	2.30 x 10 ⁻¹¹
rs35008345_C	C / C	0.06 (↑)	> 99%	3.10 x 10 ⁻¹¹
rs73212896_C	C / C	0.01 (↑)	90%	3.30 x 10 ⁻¹¹
rs57721086_T	T / T	0.02 (↑)	95%	3.40 x 10 ⁻¹¹
rs35548284_G	TTTTTTTT / TTTTTTTT	0.01 (-)	78%	3.50 x 10 ⁻¹¹
rs62162863_G	G / G	0.01 (↑)	58%	6.60 x 10 ⁻¹¹
rs11572082_C	C / C	0.01 (↑)	88%	8.00 x 10 ⁻¹¹
rs77741622_G	G / A	0.01 (↑)	65%	9.20 x 10 ⁻¹¹
rs7291444_T	T / T	0.01 (↑)	85%	9.70 x 10 ⁻¹¹
rs7618363_C	C / C	0.01 (↑)	84%	1.30 x 10 ⁻¹⁰
rs72708239_A	A / G	0.01 (↑)	74%	1.50 x 10 ⁻¹⁰
rs62314881_G	G / T	0.01 (↑)	82%	2.10 x 10 ⁻¹⁰
rs2035838_A	A / A	0.01 (↑)	85%	2.50 x 10 ⁻¹⁰
rs9543012_C	C / C	0.01 (↑)	35%	2.60 x 10 ⁻¹⁰
rs55885610_C	C / T	0.02 (↑)	96%	2.60 x 10 ⁻¹⁰
rs10202148_G	G / G	0.01 (↑)	74%	2.70 x 10 ⁻¹⁰
rs150539196_G	NA	0.02 (-)	4%	3.50 x 10 ⁻¹⁰
rs941446_T	T / T	0.01 (↑)	63%	3.50 x 10 ⁻¹⁰
rs2879910_C	C / C	0.01 (↑)	48%	4.10 x 10 ⁻¹⁰
rs62394296_T	C / T	0.01 (↑)	12%	4.20 x 10 ⁻¹⁰
rs34858588_C	C / C	0.02 (↑)	92%	4.30 x 10 ⁻¹⁰
rs35698268_G	C / C	0.01 (-)	22%	4.60 x 10 ⁻¹⁰
rs57615517_G	G / G	0.01 (↑)	69%	4.70 x 10 ⁻¹⁰
rs35222808_C	C / C	0.01 (↑)	75%	5.70 x 10 ⁻¹⁰
rs1681967_A	A / A	0.01 (↑)	92%	5.90 x 10 ⁻¹⁰
rs4961485_T	T / T	0.02 (↑)	93%	5.90 x 10 ⁻¹⁰
rs881301_T	T / T	0.01 (↑)	59%	6.40 x 10 ⁻¹⁰
rs2201003_A	A / G	0.01 (↑)	36%	6.70 x 10 ⁻¹⁰
rs72660136_T	T / T	0.02 (↑)	97%	8.50 x 10 ⁻¹⁰
rs201643157_T	C / C	0.01 (-)	25%	9.00 x 10 ⁻¹⁰
rs5763800_A	A / A	0.03 (↑)	98%	9.00 x 10 ⁻¹⁰
rs13185520_A	A / A	0.01 (↑)	57%	9.10 x 10 ⁻¹⁰
rs2764772_A	A / A	0.01 (↑)	33%	9.90 x 10 ⁻¹⁰

rs2374456_G	C / G	0.01 (↑)	59%	1.00 x 10 ⁻⁹
rs696516_G	G / G	0.01 (↑)	27%	1.10 x 10 ⁻⁹
rs10017280_C	C / C	0.01 (↑)	87%	1.20 x 10 ⁻⁹
rs11556924_T	C / T	0.01 (↑)	39%	1.20 x 10 ⁻⁹
rs4912377_C	C / A	0.01 (↑)	49%	1.40 x 10 ⁻⁹
rs113247979_T	T / T	0.05 (↑)	99%	1.50 x 10 ⁻⁹
rs6462989_A	A / A	0.01 (↑)	66%	1.50 x 10 ⁻⁹
rs733190_T	C / C	0.01 (-)	53%	1.60 x 10 ⁻⁹
rs1822246_A	A / G	0.01 (↑)	70%	1.60 x 10 ⁻⁹
rs62220604_A	G / A	0.01 (↑)	28%	1.60 x 10 ⁻⁹
rs73200740_A	C / A	0.01 (↑)	24%	1.80 x 10 ⁻⁹
rs57323441_C	A / A	0.01 (-)	12%	2.20 x 10 ⁻⁹
rs3103310_A	A / A	0.01 (↑)	76%	2.70 x 10 ⁻⁹
rs4835948_T	T / C	0.01 (↑)	53%	2.90 x 10 ⁻⁹
rs180435_G	G / G	0.01 (↑)	81%	3.00 x 10 ⁻⁹
rs2273991_G	G / G	0.01 (↑)	90%	3.00 x 10 ⁻⁹
rs494242_C	T / T	0.01 (-)	66%	3.10 x 10 ⁻⁹
rs11830764_C	G / G	0.01 (-)	7%	3.30 x 10 ⁻⁹
rs6939861_G	G / G	0.01 (↑)	74%	3.40 x 10 ⁻⁹
rs157934_C	T / T	0.01 (-)	31%	3.40 x 10 ⁻⁹
rs56271032_G	A / A	0.01 (-)	13%	3.60 x 10 ⁻⁹
rs12702516_A	C / C	0.01 (-)	15%	3.70 x 10 ⁻⁹
rs41264630_A	G / G	0.01 (-)	8%	3.90 x 10 ⁻⁹
rs2583949_C	C / C	0.01 (↑)	90%	5.00 x 10 ⁻⁹
rs535305978_C	NA	0.04 (-)	1%	5.80 x 10 ⁻⁹
rs1553668_T	T / T	0.01 (↑)	63%	6.50 x 10 ⁻⁹
rs17810415_G	A / A	0.01 (-)	20%	6.70 x 10 ⁻⁹
rs12185851_C	T / C	0.01 (↑)	23%	6.70 x 10 ⁻⁹
rs13152154_C	T / T	0.01 (-)	27%	7.30 x 10 ⁻⁹
rs2256191_T	T / C	0.01 (↑)	66%	7.40 x 10 ⁻⁹
rs11564722_T	C / T	0.01 (↑)	24%	8.20 x 10 ⁻⁹
rs12294104_T	C / C	0.01 (-)	17%	9.40 x 10 ⁻⁹
rs1782652_T	A / A	0.01 (-)	62%	9.50 x 10 ⁻⁹
rs552988313_T	T / TA	0.01 (↑)	54%	1.00 x 10 ⁻⁸
rs78461719_T	NA	0.03 (-)	3%	1.10 x 10 ⁻⁸
rs74440003_A	T / T	0.01 (-)	26%	1.10 x 10 ⁻⁸
rs2287322_G	A / G	0.01 (↑)	22%	1.10 x 10 ⁻⁸
rs445_C	C / C	0.01 (↑)	91%	1.20 x 10 ⁻⁸
rs11629457_T	T / C	0.01 (↑)	27%	1.20 x 10 ⁻⁸
rs12796488_C	C / C	0.01 (↑)	82%	1.40 x 10 ⁻⁸
rs12745935_G	A / A	0.01 (-)	30%	1.50 x 10 ⁻⁸
rs4938576_G	G / G	0.01 (↑)	59%	1.50 x 10 ⁻⁸
rs41284816_T	NA	0.03 (-)	2%	1.50 x 10 ⁻⁸
rs221584_G	A / G	0.01 (↑)	82%	1.60 x 10 ⁻⁸
rs9638084_G	G / G	0.01 (↑)	60%	1.60 x 10 ⁻⁸
rs45448191_T	T / T	0.02 (↑)	96%	2.00 x 10 ⁻⁸
rs2038695_C	C / A	0.01 (↑)	45%	2.10 x 10 ⁻⁸
rs10982192_T	C / C	0.01 (-)	22%	2.20 x 10 ⁻⁸
rs112530420_C	T / C	0.01 (↑)	17%	2.30 x 10 ⁻⁸
rs4245930_G	G / A	0.01 (↑)	37%	2.40 x 10 ⁻⁸
rs77822621_T	NA	0.02 (-)	4%	2.70 x 10 ⁻⁸
rs12788072_G	A / A	0.01 (-)	18%	2.70 x 10 ⁻⁸
rs11937496_G	G / G	0.01 (↑)	56%	2.90 x 10 ⁻⁸
rs7937758_A	A / A	0.01 (↑)	50%	2.90 x 10 ⁻⁸

rs11888201_C	C / G	0.01 (↑)	54%	3.30 x 10 ⁻⁸
rs7066171_G	C / C	0.01 (-)	66%	3.30 x 10 ⁻⁸
rs2675611_T	T / T	0.01 (↑)	47%	3.40 x 10 ⁻⁸
rs618888_T	G / G	0.01 (-)	28%	3.50 x 10 ⁻⁸
rs35182096_C	T / T	0.01 (-)	26%	3.60 x 10 ⁻⁸
rs4826631_T	C / C	0.01 (-)	71%	3.80 x 10 ⁻⁸
rs4725944_C	G / G	0.01 (-)	39%	4.60 x 10 ⁻⁸
rs9850919_C	T / T	0.01 (-)	41%	4.70 x 10 ⁻⁸
rs771258439_A	/	0.01 (-)	90%	4.70 x 10 ⁻⁸
rs12914034_A	A / A	0.01 (↑)	64%	4.70 x 10 ⁻⁸
rs78851238_C	T / T	0.01 (-)	17%	5.00 x 10 ⁻⁸

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.